

patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information including a number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point; and

comparative processing means for comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point.

2. (amended) The DNA analysis system according to claim 1, wherein the analyzing-result prediction means predicts a mass-to-charge ratio (m/z ; m is an ion mass, z is a number of electric charges) of each of the plural kinds of multiply-charged ions in each of the two cases, and the comparative processing means compares the predicted mass-to-charge ratio (m/z) of the predicted mass spectrum patterns with a mass-to-charge ratio (m/z) of the measured mass spectrum.

3. (amended) The DNA analysis system according to claim 1, wherein the analyzing-result prediction means predicts a mass-to-charge ratio (m/z ; m is an ion mass, z is the number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio (m/z) in each of the two cases, and the comparative processing means compares the predicted mass-to-charge ratio (m/z) of the predicted mass spectrum patterns with a mass-to-charge ratio (m/z) of the measured mass spectrum and compares the predicted relative ion intensities of the predicted mass spectrum patterns with relative ion intensities of the measured mass spectrum.

4. (amended) The DNA analysis system according to claim 1, further

comprising:

sampling means for supplying a sample including the test DNA fragment to the ionization means intermittently at a predetermined time period; and

detecting-output analysis means for performing the following treatment to obtain $S(i)$ for the measured mass spectrum ($I(i)$) at an ordinal number "i",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein m represents a predetermined natural number and $w(n)$ represents a factor that represents a level of influence of the sample measured at n -th before the measurement of the sample which is measured i -th, and

wherein the $S(i)$ is compared with each of the predicted mass spectrum patterns.

8. (amended) The DNA analysis system according to claim 7, further comprising:

communication means for generating information about the occurrence of the emergency .

9. (amended) The DNA analysis system according to claim 4, wherein the sampling means introduces a standard sample into the ionization means when a maximum ion intensity of the measured mass spectrum by the mass spectrometric means is smaller than a predetermined threshold.

10. (amended) The DNA analysis system according to claim 9, wherein when a maximum ion intensity of a mass spectrum of the standard sample detected by the mass spectrometric means is equal to or higher than the predetermined threshold, the sample where the maximum ion intensity of the mass spectrum is detected as one smaller than the predetermined threshold is re-supplied to the ionization means by the sampling means.

11. (amended) The DNA analysis system according to claim 9, further comprising:

a plurality of measurement systems, where each of the measurement systems comprises the sampling means, the ionization means, and the mass spectrometric means, wherein

when a maximum ion intensity of a mass spectrum of the standard sample detected by mass spectrometric means in one measurement system of the plurality of measurement systems is smaller than the predetermined threshold, the sample where a maximum ion intensity of a mass spectrum is detected as one smaller than the predetermined threshold at the one measurement system is transmitted to sampling means of another measurement system except the one measurement system.

12. (amended) The DNA analysis system according to claim 9, further comprising:

a plurality of measurement systems, where each of the measurement systems comprises the sampling means, the ionization means, and the mass spectrometric means, wherein

when a maximum ion intensity of a mass spectrum of the standard sample detected by mass spectrometric means in one measurement system of the plurality of measurement systems is smaller than the predetermined threshold, a sample intended to be measured by the one measurement system is sent to sampling means of another measurement system except the one measurement system.

Please add the following new claims:

-13. A DNA analysis system for analyzing DNA polymorphism, comprising:
sampling means for supplying a sample including a test DNA fragment to an

ionization means intermittently at a predetermined time period;

the ionization means generating plural kinds of multiply-charged ions of the test DNA fragment, where each of the multiply-charged ions has five or more charges;

mass spectrometric means for performing a mass spectrometry on the multiply-charged ions formed by the ionization means so as to measure a mass spectrum of the test DNA fragment;

detecting-output analysis means for performing the following treatment to obtain $S(i)$ for the measured mass spectrum ($I(i)$) at an ordinal number "i",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein m represents a predetermined natural number and $w(n)$ represents a factor that represents a level of influence of the sample measured at n -th before the measurement of the sample which is measured i -th;

analyzing-result prediction means that predicts possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information including a number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point, wherein the analyzing-result prediction means predicts a mass-to-charge ratio (m/z ; m is an ion mass, z is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio (m/z) in each of the two cases; and

comparative processing means for comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, wherein the comparative processing means compares the predicted mass-to-charge ratio (m/z) of the predicted mass spectrum patterns with a mass-to-charge ratio (m/z) of the measured mass spectrum and compares the predicted relative ion intensities of the predicted mass spectrum

patterns with relative ion intensities of the measured mass spectrum, and wherein the S(i) is compared with each of the predicted mass spectrum patterns.

14. A DNA analysis system for analyzing DNA polymorphism, comprising:
sampling means for supplying a sample including a test DNA fragment to an ionization means intermittently at a predetermined time period;

the ionization means generating plural kinds of multiply-charged ions of the test DNA fragment, where each of the multiply-charged ions has five or more charges;

mass spectrometric means for performing a mass spectrometry on the multiply-charged ions formed by the ionization means so as to measure a mass spectrum of the test DNA fragment;

detecting-output analysis means for performing the following treatment to obtain S(i) for the measured mass spectrum (I(i)) at an ordinal number "i",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein m represents a predetermined natural number and w(n) represents a factor that represents a level of influence of the sample measured at n-th before the measurement of the sample which is measured i-th;

analyzing-result prediction means that predicts possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information including a number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point, wherein the analyzing-result prediction means predicts a mass-to-charge ratio (m/z; m is an ion mass, z is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio (m/z) in each of the two cases; and

comparative processing means for calculating a total ion intensity of each of

the predicted mass spectrum patterns with respect to a plurality of peaks in the range of a predetermined mass-to-charge ratio (m/z) and for selecting the predicted mass spectrum pattern which has a highest total ion intensity and comparing the predicted mass spectrum patterns having the highest total ion intensity with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, and wherein the $S(i)$ is compared with the selected predicted mass spectrum patterns.

15. A DNA analysis system for analyzing DNA polymorphism, comprising:
sampling means for supplying a sample including a test DNA fragment to the ionization means intermittently at a predetermined time period;

the ionization means generating plural kinds of multiply-charged ions of the test DNA fragment, where each of the multiply-charged ions has five or more charges;

mass spectrometric means for performing a mass spectrometry on the multiply-charged ions formed by the ionization means so as to measure a mass spectrum of the test DNA fragment;

detecting-output analysis means for performing the following treatment to obtain $S(i)$ for the measured mass spectrum ($I(i)$) at an ordinal number "i",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein m represents a predetermined natural number and $w(n)$ represents a factor that represents a level of influence of the sample measured at n -th before the measurement of the sample which is measured i -th;

analyzing-result prediction means that predicts possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and the other is that the test DNA fragment is not polymorphic, based on both an information including a number of each of four different nucleic acid bases that constitutes the test DNA fragment and an

information about a polymorphism point, wherein the analyzing-result prediction means predicts a mass-to-charge ratio (m/z ; m is an ion mass, z is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio (m/z) in each of the two cases; and

comparative processing means for comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, wherein the comparative processing means selects the predicted mass spectrum pattern such that a sum of a square root of a difference between a relative intensity of the measured mass spectrum having the $S(i)$ and a relative intensity of the predicted mass spectrum pattern is smallest.

16. A DNA analysis method for analyzing DNA polymorphism, comprising the steps of:

predicting mass spectrum patterns when plural kinds of multiply-charged ions generated from a test DNA fragment, where each of the multiply-charged ions has five or more charges, in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on information of a number of each of four different nucleic acid bases that constitute the test DNA fragment and information of a polymorphism point;

generating plural kinds of multiply-charged ions from a sample containing the test DNA fragment, where each of the multiply-charged ions has five or more charges;

performing a mass spectrometry on the multiply-charged ions to measure a mass spectrum pattern;

selecting a predicted mass spectrum pattern that is most closely analogous to the measured mass spectrum pattern by comparing a plurality of the predicted mass

spectrum patterns the measured mass spectrum pattern.

17. The DNA analysis method according claim 16, wherein the selected predicted mass spectrum pattern that is most closely analogous to the measured mass spectrum pattern is selected from the predicted plural mass spectrum patterns by comparing a mass-to-charge (m/z ; m is an ion mass, z is a number of electric charges) of a peak of the measured mass spectrum pattern with a mass-to-charge (m/z) of a peak of each of the plurality of the predicted mass spectrum patterns.

18. The DNA analysis method according claim 16, wherein the selected predicted mass spectrum pattern that is most closely analogous to the measured mass spectrum pattern is selected from the predicted plural mass spectrum pattern by comparing a mass-to-charge (m/z ; m is an ion mass, z is a number of electric charges) and a distribution of an ion intensity of a peak of the measured mass spectrum pattern with a mass-to-charge (m/z) and a distribution of an ion intensity of a peak of each of the plurality of the predicted mass spectrum patterns.

19. The DNA analysis method according claim 16, wherein the steps of generating, performing and selecting are subsequently repeated, the measured mass spectrum pattern ($I(i)$) at an ordinal number " i " is subjected to the following treatment to obtain $S(i)$, and then the $S(i)$ is compared with each of the plurality of the predicted mass spectrum patterns,

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein m represents a predetermined natural number and $w(n)$ represents a factor that represents a level of influence of the sample measured at n -th before the measurement of the sample which is measured i -th.

20. The DNA analysis method according claim 16, wherein a mass

spectrum pattern of a standard sample is measured when a maximum ion intensity of the measured mass spectrum pattern is smaller than a predetermined threshold.--